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SEQUENCE LISTING

MOECKEL, Bettina BATHE, Brigitte HERMANN, Thomas PFEFFERLE, Walter BINDER, Michael

<120> Nucleotide sequences coding for the rpoB gene <130> 219774US0XCIP <140> new application <141> 2002-02-19 <150> DE 10107229.5 <151> 2001-02-16 <150> US 09/887052 <151> 2001-06-25 <160> <170> PatentIn version 3.1 <210> 1 <211> 5099 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS (702)..(4196) <222> <223> <400> acaatgtgac tcgtgatttt tgggtggatc agcgtaccgg tttggttgtc gatctagctq 60 aaaatattga tgatttttac ggcgaccgca gcggccagaa gtacgaacag aaattgcttt 120 tegacgeete cetegacgat geagetgtet etaagetggt tgeacaggee gaaageatee 180 ctgatggaga tgtgagcaaa atcgcaaata ccgtaggtat tgtgatcggt gcggtattgg 240 etetegtggg cetggeeggg tgttttgggg cgtttgggaa gaaacgtega gaagettaac 300 ctgctgttca aatagatttt ccctgtttcg aattgcggaa accccgggtt tgtttgctag 360 ggtgcctcgt agaaggggtc aagaagattt ctgggaaacg cgcccgtgcg gttggttgct 420 aatagcacgc ggagcaccag atgaaaaatc tcccctttac tttcgcgcgc gattggtata

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cgc gta acc agc ggc c Arg Val Thr Ser Gly L 70 7	eu Glu Asn Ile			
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ggt gaa atc aag tct c Gly Glu Ile Lys Ser G 135			p Phe Pro Met	
acg gac aag gga acg t Thr Asp Lys Gly Thr P 150			u Arg Val Val	
agc cag ctc gtc cgc to Ser Gln Leu Val Arg So 170				
aag tca act gag cgt co Lys Ser Thr Glu Arg P: 185				
ggt gct tgg ctt gag t Gly Ala Trp Leu Glu Pl 200				

The state of the s

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			acc Thr													1436
atc Ile	atg Met	atg Met	tcc Ser	acc Thr 250	ctc Leu	gag Glu	tcc Ser	gat Asp	ggt Gly 255	gta Val	gca Ala	aac Asn	acc Thr	gat Asp 260	gag Glu	1484
			gag Glu 265													1532
			gcg Ala													1580
			ctg Leu													1628
			ggc Gly													1676
			acc Thr													1724
			tct Ser 345													1772
			ttt Phe			_	_	_	-		_		_	_		1820
			gtc Val													1868
			acc Thr													1916
			cgt Arg													1964
			tct Ser 425													2012

Land Control of the C

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															gtg Val 965	3596
															tca Ser	3644
							Val								gca Ala	3692
		atc Ile 1000	Asp					Gl			ac cc /r Pr	о Ту		ccg Pro	_	3737
		ggc Gly 1015	Tyr					Ly			ec ca Is Hi	s Le		gtt Val	_	3782
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	gaa Glu		Glu					Gl			ıc gg r Gl	y Āl		gcc Ala		3917
aca Thr	ctt Leu	cag Gln 1075	Glu	ctg Leu	ctg Leu	acc Thr	atc Ile 108	Ly	g to s Se	t ga er As	it ga sp As	p Va	g (gtt Val		3962
cgt Arg	gtc Val	aag Lys 1090	Val	tac Tyr	gaa Glu	gca Ala	att Ile 109	Va	g aa 1 Ly	g gg s Gl	ıc ga y Gl	u As	n :	atc Ile	_	4007
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<213> Corynebacterium glutamicum

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- Ala Pro Ile Glu Val Pro Gly Leu Leu Asp Leu Gln Leu Asp Ser Tyr 35 40 45
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- Phe Gly Glu Gly Ala Arg Val Thr Ser Gly Leu Glu Asn Ile Leu Glu 65 70 75 80
- Glu Leu Ser Pro Ile Gln Asp Tyr Ser Gly Asn Met Ser Leu Ser Leu 85 90 95
- Ser Glu Pro Arg Phe Glu Asp Val Lys Asn Thr Ile Asp Glu Ala Lys
 100 105 110
- Glu Lys Asp Ile Asn Tyr Ala Ala Pro Leu Tyr Val Thr Ala Glu Phe 115 120 125
- Val Asn Asn Thr Thr Gly Glu Ile Lys Ser Gln Thr Val Phe Ile Gly 130 135 140
- Asp Phe Pro Met Met Thr Asp Lys Gly Thr Phe Ile Ile Asn Gly Thr 145 150 155 160
- Glu Arg Val Val Ser Gln Leu Val Arg Ser Pro Gly Val Tyr Phe
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- Asp Gln Thr Ile Asp Lys Ser Thr Glu Arg Pro Leu His Ala Val Lys 180 185 190
- Val Ile Pro Ser Arg Gly Ala Trp Leu Glu Phe Asp Val Asp Lys Arg 195 200 205
- Asp Ser Val Gly Val Arg Ile Asp Arg Lys Arg Arg Gln Pro Val Thr 210 215 220
- Val Leu Leu Lys Ala Leu Gly Trp Thr Thr Glu Gln Ile Thr Glu Arg 225 230 235 240

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- Ile Asn Arg Lys Leu Gly Leu Gly Gly Asp His Asp Gly Leu Met Thr 305 310 315 320
- Leu Thr Glu Glu Asp Ile Ala Thr Thr Ile Glu Tyr Leu Val Arg Leu 325 330 335
- His Ala Gly Glu Arg Val Met Thr Ser Pro Asn Gly Glu Glu Ile Pro 340 345 350
- Val Glu Thr Asp Asp Ile Asp His Phe Gly Asn Arg Arg Leu Arg Thr 355 360 365
- Val Gly Glu Leu Ile Gln Asn Gln Val Arg Val Gly Leu Ser Arg Met 370 375 380
- Glu Arg Val Val Arg Glu Arg Met Thr Thr Gln Asp Ala Glu Ser Ile 385 390 395 400
- Thr Pro Thr Ser Leu Ile Asn Val Arg Pro Val Ser Ala Ala Ile Arg 405 410 415
- Glu Phe Phe Gly Thr Ser Gln Leu Ser Gln Phe Met Asp Gln Asn Asn 420 425 430
- Ser Leu Ser Gly Leu Thr His Lys Arg Arg Leu Ser Ala Leu Gly Pro 435 440 445
- Gly Gly Leu Ser Arg Glu Arg Ala Gly Ile Glu Val Arg Asp Val His
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Pro Ser His Tyr Gly Arg Met Cys Pro Ile Glu Thr Pro Glu Gly Pro 465 470 475 480

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Phe Gly Phe Ile Glu Thr Pro Tyr Arg Arg Ile Ile Asp Gly Lys Leu 500 505 510

Thr Asp Gln Ile Asp Tyr Leu Thr Ala Asp Glu Glu Asp Arg Phe Val 515 520 525

Val Ala Gln Ala Asn Thr His Tyr Asp Glu Glu Gly Asn Ile Thr Asp 530 535 540

Glu Thr Val Thr Val Arg Leu Lys Asp Gly Asp Ile Ala Met Val Gly 545 550 555 560

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Asp Ala Gly Asp Leu Val Ile Thr Pro Val Ala Gly Val Val Glu Asn 625 630 635 640

Val Ser Ala Asp Phe Ile Thr Ile Met Ala Asp Asp Gly Lys Arg Glu 645 650 655

Thr Tyr Leu Leu Arg Lys Phe Gln Arg Thr Asn Gln Gly Thr Ser Tyr
. 660 665 670

Asn Gln Lys Pro Leu Val Asn Leu Gly Glu Arg Val Glu Ala Gly Gln 675 680 685

Val Ile Ala Asp Gly Pro Gly Thr Phe Asn Gly Glu Met Ser Leu Gly

690 695 700

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- Asp Ala Ile Ile Leu Asn Gln Asn Ile Val Glu Gln Asp Ile Leu Thr
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- Ser Ile His Ile Glu Glu His Glu Ile Asp Ala Arg Asp Thr Lys Leu 740 745 750
- Gly Ala Glu Glu Ile Thr Arg Asp Ile Pro Asn Val Ser Glu Glu Val
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- Leu Lys Asp Leu Asp Asp Arg Gly Ile Val Arg Ile Gly Ala Asp Val 770 780
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- Gly Lys Val Ile Gly Val Arg His Phe Ser Arg Glu Asp Asp Asp Asp 835 840 845
- Leu Ala Pro Gly Val Asn Glu Met Ile Arg Ile Tyr Val Ala Gln Lys 850 855 860
- Arg Lys Ile Gln Asp Gly Asp Lys Leu Ala Gly Arg His Gly Asn Lys 865 870 875 880
- Gly Val Val Gly Lys Ile Leu Pro Gln Glu Asp Met Pro Phe Leu Pro 885 890 895
- Asp Gly Thr Pro Val Asp Ile Ile Leu Asn Thr His Gly Val Pro Arg 900 905 910
- Arg Met Asn Ile Gly Gln Val Leu Glu Thr His Leu Gly Trp Leu Ala 915 920 925

- Ser Ala Gly Trp Ser Val Asp Pro Glu Asp Pro Glu Asn Ala Glu Leu 930 935 940
- Val Lys Thr Leu Pro Ala Asp Leu Leu Glu Val Pro Ala Gly Ser Leu 945 950 955 960
- Thr Ala Thr Pro Val Phe Asp Gly Ala Ser Asn Glu Glu Leu Ala Gly 965 970 975
- Leu Leu Ala Asn Ser Arg Pro Asn Arg Asp Gly Asp Val Met Val Asn 980 985 990
- Ala Asp Gly Lys Ala Thr Leu Ile Asp Gly Arg Ser Gly Glu Pro Tyr 995 1000 1005
- Pro Tyr Pro Val Ser Ile Gly Tyr Met Tyr Met Leu Lys Leu His 1010 1015 1020
- His Leu Val Asp Glu Lys Ile His Ala Arg Ser Thr Gly Pro Tyr 1025 1030 1035
- Ser Met Ile Thr Gln Gln Pro Leu Gly Gly Lys Ala Gln Phe Gly 1040 1045 1050
- Gly Gln Arg Phe Gly Glu Met Glu Val Trp Ala Met Gln Ala Tyr 1055 1060 1065
- Gly Ala Ala Tyr Thr Leu Gln Glu Leu Leu Thr Ile Lys Ser Asp 1070 1080
- Asp Val Val Gly Arg Val Lys Val Tyr Glu Ala Ile Val Lys Gly 1085 1090 1095
- Glu Asn Ile Pro Asp Pro Gly Ile Pro Glu Ser Phe Lys Val Leu 1100 1105 1110
- Leu Lys Glu Leu Gln Ser Leu Cys Leu Asn Val Glu Val Leu Ser 1115 1120 1125
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Application of the second

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gtg Val	cgt Arg	cac His 840	ttc Phe	tcc Ser	cgc Arg	gag Glu	gac Asp 845	gac Asp	gac Asp	gat Asp	ctg Leu	gct Ala 850	cct Pro	ggc Gly	gtc Val	3260
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ggc																

The state of the s

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gac Asp	atc Ile	atc Ile	ttg Leu 905	aac Asn	acc Thr	cac His	ggt Gly	gtt Val 910	cca Pro	cgt Arg	cgt Arg	atg a Met A 9	ac a sn I 15	itt (ggt Gly	3452
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cgt Arg	gtc Val	aag Lys 1090	Val	tac Tyr	gaa Glu	gca Ala	att Ile 109	Va	g aa l Ly	g gg s Gl;	cʻgaq y Gli	g aac u Asn 1100	Ιlε	c cc e Pr	_	4007
gat	cca	ggt	att	cct	gag	tcc	ttc	aa	g gt	t ct	c cto	aag	gag	g ct	С	4052

स्ति देश कर्म क्षेत्र ।

Asp Pro G	los	Giu ser P	ne Lys .110	Val Le	u Leu Lys 111		1
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- Ser Trp Leu Ile Gly Thr Pro Glu Trp Arg Ala Arg Gln Lys Glu Glu 50 55 60
- Phe Gly Glu Gly Ala Arg Val Thr Ser Gly Leu Glu Asn Ile Leu Glu 65 70 75 80
- Glu Leu Ser Pro Ile Gln Asp Tyr Ser Gly Asn Met Ser Leu Ser Leu 85 90 95
- Ser Glu Pro Arg Phe Glu Asp Val Lys Asn Thr Ile Asp Glu Ala Lys
 100 105 110
- Glu Lys Asp Ile Asn Tyr Ala Ala Pro Leu Tyr Val Thr Ala Glu Phe
 115 120 125
- Val Asn Asn Thr Thr Gly Glu Ile Lys Ser Gln Thr Val Phe Ile Gly 130 135 140
- Asp Phe Pro Met Met Thr Asp Lys Gly Thr Phe Ile Ile Asn Gly Thr 145 150 155 160
- Glu Arg Val Val Ser Gln Leu Val Arg Ser Pro Gly Val Tyr Phe
 165 170 175
- Asp Gln Thr Ile Asp Lys Ser Thr Glu Arg Pro Leu His Ala Val Lys 180 185 190
- Val Ile Pro Phe Arg Gly Ala Trp Leu Glu Phe Asp Val Asp Lys Arg . 195 200 205
- Asp Ser Val Gly Val Arg Ile Asp Arg Lys Arg Arg Gln Pro Val Thr 210 215 220
- Val Leu Leu Lys Ala Leu Gly Trp Thr Thr Glu Gln Ile Thr Glu Arg

Phe Gly Phe Ser Glu Ile Met Met Ser Thr Leu Glu Ser Asp Gly Val 245 250 255

Ala Asn Thr Asp Glu Ala Leu Leu Glu Ile Tyr Arg Lys Gln Arg Pro 260 265 270

Gly Glu Gln Pro Thr Arg Asp Leu Ala Gln Ser Leu Leu Asp Asn Ser 275 280 285

Phe Phe Arg Ala Lys Arg Tyr Asp Leu Ala Arg Val Gly Arg Tyr Lys 290 295 300

Ile Asn Arg Lys Leu Gly Leu Gly Gly Asp His Asp Gly Leu Met Thr 305 310 315 320

Leu Thr Glu Glu Asp Ile Ala Thr Thr Ile Glu Tyr Leu Val Arg Leu 325 330 335

His Ala Gly Glu Arg Val Met Thr Ser Pro Asn Gly Glu Glu Ile Pro 340 345 350

Val Glu Thr Asp Asp Ile Asp His Phe Gly Asn Arg Arg Leu Arg Thr 355 360 365

Val Gly Glu Leu Ile Gln Asn Gln Val Arg Val Gly Leu Ser Arg Met 370 375 380

Glu Arg Val Val Arg Glu Arg Met Thr Thr Gln Asp Ala Glu Ser Ile 385 390 395 400

Thr Pro Thr Ser Leu Ile Asn Val Arg Pro Val Ser Ala Ala Ile Arg 405 410 415

Glu Phe Phe Gly Thr Ser Gln Leu Ser Gln Phe Met Val Gln Asn Asn 420 425 430

Ser Leu Ser Gly Leu Thr His Lys Arg Arg Leu Ser Ala Leu Gly Pro 435 440 445

Gly Gly Leu Ser Arg Glu Arg Ala Gly Ile Glu Val Arg Asp Val His 450 455 460

470 475 Asn Ile Gly Leu Ile Gly Ser Leu Ala Ser Tyr Ala Arg Val Asn Pro Phe Gly Phe Ile Glu Thr Pro Tyr Arg Ile Ile Asp Gly Lys Leu 505 Thr Asp Gln Ile Asp Tyr Leu Thr Ala Asp Glu Glu Asp Arg Phe Val 520 Val Ala Gln Ala Asn Thr His Tyr Asp Glu Glu Gly Asn Ile Thr Asp 535 Glu Thr Val Thr Val Arg Leu Lys Asp Gly Asp Ile Ala Met Val Gly 550 555 560 Arg Asn Ala Val Asp Tyr Met Asp Val Ser Pro Arg Gln Met Val Ser 570 575 Val Gly Thr Ala Met Ile Pro Phe Leu Glu His Asp Asp Ala Asn Arg 580 585 Ala Leu Met Gly Ala Asn Met Gln Lys Gln Ala Val Pro Leu Ile Arq 595 600 Ala Glu Ala Pro Phe Val Gly Thr Gly Met Glu Gln Arg Ala Ala Tyr 610 Asp Ala Gly Asp Leu Val Ile Thr Pro Val Ala Gly Val Val Glu Asn 625 Val Ser Ala Asp Phe Ile Thr Ile Met Ala Asp Asp Gly Lys Arg Glu 645 Thr Tyr Leu Leu Arg Lys Phe Gln Arg Thr Asn Gln Gly Thr Ser Tyr

Asn Gln Lys Pro Leu Val Asn Leu Gly Glu Arg Val Glu Ala Gly Gln

660

675

Pro Ser His Tyr Gly Arg Met Cys Pro Ile Glu Thr Pro Glu Gly Pro

- Val Ile Ala Asp Gly Pro Gly Thr Phe Asn Gly Glu Met Ser Leu Gly 690 695 700
- Arg Asn Leu Leu Val Ala Phe Met Pro Trp Glu Gly His Asn Tyr Glu 705 710 715 720
- Asp Ala Ile Ile Leu Asn Gln Asn Ile Val Glu Gln Asp Ile Leu Thr 725 730 735
- Ser Ile His Ile Glu Glu His Glu Ile Asp Ala Arg Asp Thr Lys Leu 740 745 750
- Gly Ala Glu Glu Ile Thr Arg Asp Ile Pro Asn Val Ser Glu Glu Val 755 760 765
- Leu Lys Asp Leu Asp Asp Arg Gly Ile Val Arg Ile Gly Ala Asp Val 770 780
- Arg Asp Gly Asp Ile Leu Val Gly Lys Val Thr Pro Lys Gly Glu Thr 785 790 795 800
- Glu Leu Thr Pro Glu Glu Arg Leu Leu Arg Ala Ile Phe Gly Glu Lys 805 810 815
- Ala Arg Glu Val Arg Asp Thr Ser Met Lys Val Pro His Gly Glu Thr 820 825 830
- Gly Lys Val Ile Gly Val Arg His Phe Ser Arg Glu Asp Asp Asp Asp 835 840 845
- Leu Ala Pro Gly Val Asn Glu Met Ile Arg Ile Tyr Val Ala Gln Lys 850 855 860
- Arg Lys Ile Gln Asp Gly Asp Lys Leu Ala Gly Arg His Gly Asn Lys 865 870 875 880
- Gly Val Val Gly Lys Ile Leu Pro Gln Glu Asp Met Pro Phe Leu Pro 885 890 895
- Asp Gly Thr Pro Val Asp Ile Ile Leu Asn Thr His Gly Val Pro Arg 900 905 910

- Arg Met Asn Ile Gly Gln Val Leu Glu Thr His Leu Gly Trp Leu Ala 915 920 925
- Ser Ala Gly Trp Ser Val Asp Pro Glu Asp Pro Glu Asn Ala Glu Leu 930 935 940
- Val Lys Thr Leu Pro Ala Asp Leu Leu Glu Val Pro Ala Gly Ser Leu 945 950 955 960
- Thr Ala Thr Pro Val Phe Asp Gly Ala Ser Asn Glu Glu Leu Ala Gly 965 970 975
- Leu Leu Ala Asn Ser Arg Pro Asn Arg Asp Gly Asp Val Met Val Asn 980 985 990
- Ala Asp Gly Lys Ala Thr Leu Ile Asp Gly Arg Ser Gly Glu Pro Tyr 995 1000 1005
- Pro Tyr Pro Val Ser Ile Gly Tyr Met Tyr Met Leu Lys Leu His 1010 1015 1020
- His Leu Val Asp Glu Lys Ile His Ala Arg Ser Thr Gly Pro Tyr 1025 1030 1035
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- Gly Gln Arg Phe Gly Glu Met Glu Val Trp Ala Met Gln Ala Tyr 1055 1060 1065
- Gly Ala Ala Tyr Thr Leu Gln Glu Leu Leu Thr Ile Lys Ser Asp 1070 1075 1080
- Asp Val Val Gly Arg Val Lys Val Tyr Glu Ala Ile Val Lys Gly 1085 1090 1095
- Glu Asn Ile Pro Asp Pro Gly Ile Pro Glu Ser Phe Lys Val Leu 1100 1105 1110
- Leu Lys Glu Leu Gln Ser Leu Cys Leu Asn Val Glu Val Leu Ser 1115 1120 1125
- Ala Asp Gly Thr Pro Met Glu Leu Ala Gly Asp Asp Asp Phe

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<223>

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<222> (2016)..(2016)

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			ctt Leu								860
			gct Ala								908
			ctt Leu 75								956
			aac Asn								1004
			acc Thr								1052
			tat Tyr								1100
			cag Gln								1148
			ttc Phe 155								1196
	_	_	tcc Ser	_	 		_	_		_	1244
			cca Pro								1292
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			cgt Arg								1388
			gag Glu 235								1436

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														cct Pro		1532
														gca Ala		1580
_		_	_	_	_	_		_		_			_	aag Lys		1628
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The state of the state of

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	tcc Ser															2204
	cca Pro															2252
	ctt Leu															2300
	cac His 535															2348
	ctg Leu															2396
	atg Met															2444
	cca Pro															2492
	atg Met															2540
	ggc Gly 615															2588
gtt Val 630	att Ile	acc Thr	cca Pro	gtc Val	gca Ala 635	ggt Gly	gtg Val	gtg Val	gaa Glu	aac Asn 640	gtt Val	tca Ser	gct Ala	gac Asp	ttc Phe 645	2636
	acc Thr															2684
	ttc Phe															2732
	aac Asn															2780
cca	ggt	acc	ttc	aat	ggt	gaa	atg	tcc	ctt	ggc	cgţ	aac	ctt	ctg	gtt	2828

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gag Glu	cac His	gag Glu	atc Ile 745	gat Asp	gcc Ala	cgc Arg	gac Asp	act Thr 750	aag Lys	ctt Leu	ggc Gly	gcc Ala	gaa Glu 755	gaa Glu	atc Ile	2972
								gaa Glu								3020
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ctg Leu 790	gtc Val	ggt Gly	aag Lys	gtc Val	acc Thr 795	cct Pro	aag Lys	ggc Gly	gag Glu	acc Thr 800	gag Glu	ctc Leu	acc Thr	ccg Pro	gaa Glu 805	3116
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920	925	930

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		cag Gln 1075	Glu				atc Ile 1080	Lys					_	ggc Gly	:	3962
_	_	aag Lys 1090					att Ile 1095	Val						ccg Pro	4	4007
		ggt Gly 1105	att Ile	cct Pro	gag Glu	tcc Ser	ttc Phe 1110	Lys	gtt Val	t cto L Lei	ctc Leu	aag Lys 1115	gag Glu	ctc Leu	4	4052
cag Gln	tcc Ser	ttg Leu 1120	tgc Cys	ctg Leu	aac Asn	gtg Val	gag Glu 1125	Val	cto Lei	c tco ı Sei	gca Ala	gac Asp 1130	ggc Gly	act Thr	4	1097
		gag Glu 1135					gac Asp 1140	Asp				cag Gln 1145	gca Ala	ggc Gly	4	1142

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gac acc gca Asp Thr Ala .1165	tagcagato	ca gaaaacaad	cc gctagaaat	c aagccatad	ca	4236
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Ala Pro Ile Glu Val Pro Gly Leu Leu Asp Leu Gln Leu Asp Ser Tyr 40 _ 45

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<213> Corynebacterium glutamicum

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Phe Gly Glu Gly Ala Arg Val Thr Ser Gly Leu Glu Asn Ile Leu Glu 65 70 75 80

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Ser Glu Pro Arg Phe Glu Asp Val Lys Asn Thr Ile Asp Glu Ala Lys 100 105 110

Glu Lys Asp Ile Asn Tyr Ala Ala Pro Leu Tyr Val Thr Ala Glu Phe 115 120 125

Val Asn Asn Thr Thr Gly Glu Ile Lys Ser Gln Thr Val Phe Ile Gly 130 135 140

Asp Phe Pro Met Met Thr Asp Lys Gly Thr Phe Ile Ile Asn Gly Thr 145 150 155 160

Glu Arg Val Val Ser Gln Leu Val Arg Ser Pro Gly Val Tyr Phe 165 170 175

Asp Gln Thr Ile Asp Lys Ser Thr Glu Arg Pro Leu His Ala Val Lys 180 185 190

Val Ile Pro Ser Arg Gly Ala Trp Leu Glu Phe Asp Val Asp Lys Arg 195 200 205

Asp Ser Val Gly Val Arg Ile Asp Arg Lys Arg Arg Gln Pro Val Thr 210 215 220

Val Leu Leu Lys Ala Leu Gly Trp Thr Thr Glu Gln Ile Thr Glu Arg 225 230 235 240

Phe Gly Phe Ser Glu Ile Met Met Ser Thr Leu Glu Ser Asp Gly Val 245 250 255

Ala Asn Thr Asp Glu Ala Leu Leu Glu Ile Tyr Arg Lys Gln Arg Pro 260 265 270

- Gly Glu Gln Pro Thr Arg Asp Leu Ala Gln Ser Leu Leu Asp Asn Ser 275 280 285
- Phe Phe Arg Ala Lys Arg Tyr Asp Leu Ala Arg Val Gly Arg Tyr Lys 290 295 300
- Ile Asn Arg Lys Leu Gly Leu Gly Gly Asp His Asp Gly Leu Met Thr 305 310 315 320
- Leu Thr Glu Glu Asp Ile Ala Thr Thr Ile Glu Tyr Leu Val Arg Leu 325 330 335
- His Ala Gly Glu Arg Val Met Thr Ser Pro Asn Gly Glu Glu Ile Pro 340 345 350
- Val Glu Thr Asp Asp Ile Asp His Phe Gly Asn Arg Arg Leu Arg Thr 355 360 365
- Val Gly Glu Leu Ile Gln Asn Gln Val Arg Val Gly Leu Ser Arg Met 370 375 380
- Glu Arg Val Val Arg Glu Arg Met Thr Thr Gln Asp Ala Glu Ser Ile 385 390 395 400
- Thr Pro Thr Ser Leu Ile Asn Val Arg Pro Val Ser Ala Ala Ile Arg 405 410 415
- Glu Phe Phe Gly Thr Ser Gln Leu Ser Gln Phe Met Asp Gln Asn Asn 420 425 430
- Ser Leu Ser Gly Leu Thr Tyr Lys Arg Arg Leu Ser Ala Leu Gly Pro 435 440 445
- Gly Gly Leu Ser Arg Glu Arg Ala Gly Ile Glu Val Arg Asp Val His 450 455 460
- Pro Ser His Tyr Gly Arg Met Cys Pro Ile Glu Thr Pro Glu Gly Pro 465 470 475 480
- Asn Ile Gly Leu Ile Gly Ser Leu Ala Ser Tyr Ala Arg Val Asn Pro 485 490 495

• 1 -- -- -- --

- Phe Gly Phe Ile Glu Thr Pro Tyr Arg Arg Ile Ile Asp Gly Lys Leu 500 505 510
- Thr Asp Gln Ile Asp Tyr Leu Thr Ala Asp Glu Glu Asp Arg Phe Val 515 520 525
- Val Ala Gln Ala Asn Thr His Tyr Asp Glu Glu Gly Asn Ile Thr Asp 530 535 540
- Glu Thr Val Thr Val Arg Leu Lys Asp Gly Asp Ile Ala Met Val Gly 545 550 555 560
- Arg Asn Ala Val Asp Tyr Met Asp Val Ser Pro Arg Gln Met Val Ser 565 570 575
- Val Gly Thr Ala Met Ile Pro Phe Leu Glu His Asp Asp Ala Asn Arg 580 585 590
- Ala Leu Met Gly Ala Asn Met Gln Lys Gln Ala Val Pro Leu Ile Arg 595 600 605
- Ala Glu Ala Pro Phe Val Gly Thr Gly Met Glu Gln Arg Ala Ala Tyr 610 615 620 .
- Asp Ala Gly Asp Leu Val Ile Thr Pro Val Ala Gly Val Val Glu Asn 625 630 635
- Val Ser Ala Asp Phe Ile Thr Ile Met Ala Asp Asp Gly Lys Arg Glu 645 650 655
- Thr Tyr Leu Leu Arg Lys Phe Gln Arg Thr Asn Gln Gly Thr Ser Tyr 660 665 670
- Asn Gln Lys Pro Leu Val Asn Leu Gly Glu Arg Val Glu Ala Gly Gln 675 680 685
- Val Ile Ala Asp Gly Pro Gly Thr Phe Asn Gly Glu Met Ser Leu Gly 690 695 700
- Arg Asn Leu Leu Val Ala Phe Met Pro Trp Glu Gly His Asn Tyr Glu 705 710 715 720
- Asp Ala Ile Ile Leu Asn Gln Asn Ile Val Glu Gln Asp Ile Leu Thr

Ser Ile His Ile Glu Glu His Glu Ile Asp Ala Arg Asp Thr Lys Leu 740 745 750

- Gly Ala Glu Glu Ile Thr Arg Asp Ile Pro Asn Val Ser Glu Glu Val
 755 760 765
- Leu Lys Asp Leu Asp Asp Arg Gly Ile Val Arg Ile Gly Ala Asp Val 770 780
- Arg Asp Gly Asp Ile Leu Val Gly Lys Val Thr Pro Lys Gly Glu Thr 785 790 795 800
- Glu Leu Thr Pro Glu Glu Arg Leu Leu Arg Ala Ile Phe Gly Glu Lys 805 810 815
- Ala Arg Glu Val Arg Asp Thr Ser Met Lys Val Pro His Gly Glu Thr 820 825 830
- Gly Lys Val Ile Gly Val Arg His Phe Ser Arg Glu Asp Asp Asp Asp 835 840 845
- Leu Ala Pro Gly Val Asn Glu Met Ile Arg Ile Tyr Val Ala Gln Lys 850 855 860
- Arg Lys Ile Gln Asp Gly Asp Lys Leu Ala Gly Arg His Gly Asn Lys 865 870 875 880
- Gly Val Val Gly Lys Ile Leu Pro Gln Glu Asp Met Pro Phe Leu Pro 885 890 895
- Asp Gly Thr Pro Val Asp Ile Ile Leu Asn Thr His Gly Val Pro Arg 900 905 910
- Arg Met Asn Ile Gly Gln Val Leu Glu Thr His Leu Gly Trp Leu Ala 915 920 925
- Ser Ala Gly Trp Ser Val Asp Pro Glu Asp Pro Glu Asn Ala Glu Leu 930 935 940
- Val Lys Thr Leu Pro Ala Asp Leu Leu Glu Val Pro Ala Gly Ser Leu 945 950 955 960

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- Thr Ala Thr Pro Val Phe Asp Gly Ala Ser Asn Glu Glu Leu Ala Gly 965 970 975
- Leu Leu Ala Asn Ser Arg Pro Asn Arg Asp Gly Asp Val Met Val Asn 980 985 990
- Ala Asp Gly Lys Ala Thr Leu Ile Asp Gly Arg Ser Gly Glu Pro Tyr 995 1000 1005
- Pro Tyr Pro Val Ser Ile Gly Tyr Met Tyr Met Leu Lys Leu His 1010 1015 1020
- His Leu Val Asp Glu Lys Ile His Ala Arg Ser Thr Gly Pro Tyr 1025 1030 1035
- Gly Gln Arg Phe Gly Glu Met Glu Val Trp Ala Met Gln Ala Tyr 1055 1060 1065
- Gly Ala Ala Tyr Thr Leu Gln Glu Leu Leu Thr Ile Lys Ser Asp 1070 1080
- Asp Val Val Gly Arg Val Lys Val Tyr Glu Ala Ile Val Lys Gly 1085 1090 1095
- Glu Asn Ile Pro Asp Pro Gly Ile Pro Glu Ser Phe Lys Val Leu 1100 1105 1110
- Leu Lys Glu Leu Gln Ser Leu Cys Leu Asn Val Glu Val Leu Ser 1115 1120 1125
- Ala Asp Gly Thr Pro Met Glu Leu Ala Gly Asp Asp Asp Phe 1130 1135 1140
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tegg	gttaa	agg 1	tcag	tggc	ga g	cttc	tttg	c tg	gttc	gttt	cct	tgag	gaa	cagt	catggg	180
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														ggt Gly		580
cct Pro	cag Gln	cgt Arg 30	cgt Arg	ggc Gly	gta Val	tgc Cys	acc Thr 35	cgt Arg	gtg Val	tac Tyr	acc Thr	acc Thr 40	acc Thr	cct Pro	aag Lys	628
aag Lys														acc Thr		676
ggc Gly 60														ctg Leu		724
gag Glu																772
ggt Gly	gtc Val	cgt Arg	tac Tyr 95	aag Lys	atc Ile	gtc Val	cgt Arg	ggc Gly	gca Ala	ctg Leu	gat Asp	acc Thr	cag Gln	ggt Gly	gtt Val	820

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Val Cys Thr Arg Val Tyr Thr Thr Thr Pro Lys Lys Pro Asn Ser Ala 35 40 45

Ala Tyr Ile Pro Gly Glu Gly His Asn Leu Gln Glu His Ser Met Val Leu Val Arg Gly Gly Arg Val Lys Asp Leu Pro Gly Val Arg Tyr Lys Ile Val Arg Gly Ala Leu Asp Thr Gln Gly Val Lys Asp Arg Lys Gln Ala Arg Ser Pro Leu Arg Arg Glu Glu Gly Ile Ile Lys Asn Ala 120 <210> 9 <211> 24 <212> DNA <213> ARTIFICIAL SEQUENCE <220> <223> SYNTHETIC DNA <400> 9 acaatgtgac tcgtgatttt tggg 24 <210> 10 <211> 20 <212> DNA <213> ARTIFICIAL SEQUENCE <220> <223> SYNTHETIC DNA <400> 10 ggaaacgtcc atgtaatcaa 20 <210> 11 <211> 20 <212> DNA <213> ARTIFICIAL SEQUENCE <220> <223> SYNTHETIC DNA

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